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☐ 1: Appl Microbiol Biotechnol. 1993 Jan;38(4):493-501.

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Cloning and molecular analysis of the poly(3-hydroxybutyric acid) biosynthetic genes of *Thiocystis violacea*.

Liebergesell M, Steinbuechel A.

Institut für Mikrobiologie, Georg-August-Universität Göttingen, Federal Republic of Germany.

From a genomic library of *Thiocystis violacea* strain 2311 in lambda L47, two adjacent EcoRI restriction fragments of 5361 base pairs (bp) and of 1978 bp were cloned. The 5361-bp EcoRI restriction fragment hybridized with a DNA fragment harbouring the *Alcaligenes eutrophus* poly(3-hydroxyalkanoate) (PHA) synthase operon (*phbCAB*) and restored the ability to synthesize and accumulate PHA in PHA-negative mutants derived from *A. eutrophus*. The nucleotide sequence analysis of both fragments revealed five open-reading frames (ORFs); at least three of them are probably relevant for PHA biosynthesis. The amino acid sequences of the putative proteins deduced from these genes indicate that they encode a beta-ketothiolase [*phbATv*, relative molecular mass (*M*(r)) 40850], which exhibited 87.3% amino acid identity with the beta-ketothiolase from *Chromatium vinosum*. The amino acid sequences of the putative proteins deduced from ORF2Tv (*M*(r) 41450) and *phbCTv* (*M*(r) 39550), which were located upstream of and antilinear to *phbATv*, exhibited 74.7% and 87.6% amino acid identity, respectively, with the corresponding gene products of *C. vinosum*. Downstream of and antilinear to *phbCTv* was located ORF5, which encodes for a protein of high relative molecular mass (*M*(r) 76428) of unknown function. With respect to the divergent organisation of ORF2Tv and *phbCTv* on one side and of *phbATv* on the other side and from the homologies of the putative gene products, this region of the *T. violacea* genome resembled very much the corresponding region of *C. vinosum*, which was identified recently.

PMID: 7763384 [PubMed - indexed for MEDLINE]

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